

c). Remarks

Claim 4 is amended in order to even better distinguish the present invention from the prior art. No new matter has been added.

In the previous office Action, claim 7 is allowed. Claims 4-6, 8, 9 and 11-13 are rejected for the reasons discussed below, and claims 3, 10 and 14 are withdrawn from consideration as being directed towards a non-elected invention.

In response, the allowance of claim 7 is acknowledged. The Examiner's assistance and cooperation in expediting the allowance of this application by separately examining Applicants' various claims is gratefully appreciated. With regard to claims 10 and 14, rejoinder of the same is respectfully requested upon the allowance of antecedent claims 4 or 11. MPEP §821.04.

Withdrawn claim 3 has been cancelled in order to reduce the issues presented herein.

At the outset, regarding a formal matter, the paper copy and computer readable form of the Sequence Listing filed February 23, 2004 contained a typographical error: in the information for SEQ ID NO:1, the cleavage site feature said to be at "5927 to 5032" (see page 2 of the paper copy, 8th line from the bottom) should have read --5027-5032--. Such has been corrected in the attached Submission of Sequence Listing.

The Examiner states that neither PCT/JP96/03862 nor Japanese application No. 1995-343700/95 disclose SEQ ID NOS: 1 and 2 and has provided no priority benefit to the same. First as to PCT/JP96/03862, the Examiner's analysis is incorrect.

PCT/JP96/03862 was filed December 27, 1996 and was published on July 10, 1997 as WO 97/24442. As shown in the attached pages 20 to 40 of WO 97/24442 (“WO ‘442”) at Tab B, SEQ ID NO:1 of WO ‘442 is identical to SEQ ID NO:1 of record herein. Moreover, as seen in those sheets, SEQ ID NO:2 of record herein is also identical to the amino acid sequence provided in SEQ ID NO:1 of WO ‘442.

As to Japanese patent application No. 1995-343700, the sequences therein contained some minor typographical errors. While Applicants can properly establish the inherency of the correction of such errors by Declaration under Rule 132, such is not thought to be necessary in view of the state of the prior art. Accordingly, it is simply noted that a certified copy of the Japanese application has been filed with the PCT and Applicants reserve their right to conclusively show that the subject matter of the pending claims is supported in the Japanese application, if the state of the prior art later requires doing so.

The Examiner has requested that the continuing parent lineage be updated to reflect the status of earlier-filed U.S. application No. 08/894,344. Such has been attended to above.

The Examiner has also objected to the specification because of the phrase “sequence represented by” and Applicants’ use of the term “DNAs.” At the outset, the undersigned wishes to explain on the record that, whatever the Examiner’s personal preference may be, such are very well-accepted by the USPTO.^{1/} Accordingly, such objections are not well-understood. Moreover, in any event, it is understood that examination

^{1/} Witness 2772 patents issued containing “sequence represented by” since 1976, and 14,662 patents issued containing “DNAs”.

is not made for the purpose of securing grammatical perfection (MPEP §608.01(g)), rather, Applicants are permitted to utilize their own terminology as long as it can be understood (id). Plainly, the terminology objected to by the Examiner is eminently understandable.^{2/} Indeed, such is utilized in issued parent U.S. Patent No. 6,172,196.

In any event, it is incumbent upon the Examiner to recognize specification may, as here, no longer be available electronically and that the burden incurred in compliance is frequently onerous. Nonetheless, despite all the above, the undersigned has sought above to comply with the Examiner's request.

Claim 4 stands rejected under 35 USC §112, second paragraph, for improper dependency. In response, claim 4 is amended to correct this deficiency.

Claims 4-6, 8, 9 and 11-13 are rejected under 35 USC §112, first paragraph, for lack of written description and/or as not being supported by an enabling disclosure. These rejections are respectfully traversed. However, solely in order to reduce the issues and expedite prosecution herein, claim 4 has been amended in order to address the examiner's concerns.

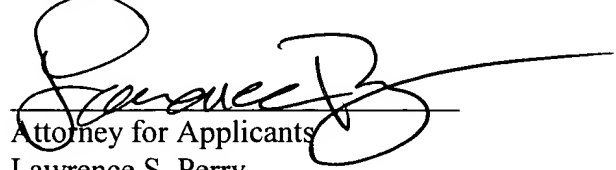
In view of the above amendments and remarks, Applicants submit that all of the Examiner's concerns are now overcome and the claims are now in allowable condition. Accordingly, reconsideration and allowance of this application is earnestly solicited.

Claims 4-14 remain presented for continued prosecution, claim 7 having been allowed with claims 4-6, 8, 9 and 11-13 now being in allowable condition and rejoinder of claims 10 and 14 being earnestly solicited.

^{2/} Or at least the Examiner has made no showing why it is not.

Applicants' undersigned attorney may be reached in our New York office by telephone at (212) 218-2100. All correspondence should continue to be directed to our below listed address.

Respectfully submitted,

A handwritten signature in black ink, appearing to read "Lawrence S. Perry", is written over a horizontal line.

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【配列表】

配列番号：1

配列の長さ：8874

配列の型：核酸

鎖の数：二本鎖

トポロジー：直鎖状

配列種類：Genomic DNA

起源

生物名：サッカロミセス セルビジェ (Saccharomyces cerevisiae)

株名：X2180-1B

配列の特徴

特徴を表す記号：CDS

存在位置：1..8874

特徴を決定した方法：E

配列の特徴

特徴を表す記号：cleavage-site

存在位置：1291..1296

特徴を決定した方法：S

配列の特徴

特徴を表す記号：cleavage-site

存在位置：4388..4393

特徴を決定した方法：S

配列の特徴

特徴を表す記号：cleavage-site

存在位置：5027..5032

特徴を決定した方法：S

配列の特徴

特徴を表す記号：cleavage-site

存在位置：7675..7680

特徴を決定した方法：S

配列

ATG GAA GCT ATT TCA CAA TTA CGT GGT GTT CCA TTG ACA CAC CAA AAG	48
Met Glu Ala Ile Ser Gln Leu Arg Gly Val Pro Leu Thr His Gln Lys	
1 5 10 15	
GAC TTT AGC TGG GTC TTT TTA GTA GAT TGG ATT CTC ACG GTA GTA GTA	96
Asp Phe Ser Trp Val Phe Leu Val Asp Trp Ile Leu Thr Val Val Val	
20 25 30	
TGT TTG ACA ATG ATA TTC TAC ATG GGA AGA ATC TAT GCA TAC CTT GTA	144
Cys Leu Thr Met Ile Phe Tyr Met Gly Arg Ile Tyr Ala Tyr Leu Val	
35 40 45	
AGT TTT ATA TTA GAA TGG CTA CTA TGG AAA CGA GCG AAA ATC AAG ATA	192
Ser Phe Ile Leu Glu Trp Leu Leu Trp Lys Arg Ala Lys Ile Lys Ile	
50 55 60	
AAT GTT GAG ACA CTT CGT GTC TCC TTA CTA GGT GGT CGA ATA CAT TTT	240
Asn Val Glu Thr Leu Arg Val Ser Leu Leu Gly Gly Arg Ile His Phe	
65 70 75 80	
AAA AAC CTT TCC GTA ATA CAC AAA GAT TAT ACA ATT TCG GTA TTA GAG	288
Lys Asn Leu Ser Val Ile His Lys Asp Tyr Thr Ile Ser Val Leu Glu	
85 90 95	
GGT AGT TTA ACA TGG AAA TAC TGG CTT TTA AAT TGC AGA AAA GCA GAA	336
Gly Ser Leu Thr Trp Lys Tyr Trp Leu Leu Asn Cys Arg Lys Ala Glu	
100 105 110	
TTG ATA GAG AAT AAC AAG TCT TCT TCT GGC AAA AAA GCA AAG CTT CCC	384
Leu Ile Glu Asn Asn Lys Ser Ser Ser Gly Lys Lys Ala Lys Leu Pro	
115 120 125	
TGT AAA ATT TCC GTA GAA TGT GAA GGT CTA GAA ATT TTT ATT TAC AAC	432
Cys Lys Ile Ser Val Glu Cys Glu Gly Leu Glu Ile Phe Ile Tyr Asn	
130 135 140	

AGA ACA GTG GCG TAC GAT AAT GTT ATA AAC TTA CTA TCA AAA GAT GAA 480
 Arg Thr Val Ala Tyr Asp Asn Val Ile Asn Leu Leu Ser Lys Asp Glu
 145 150 155 160
 CGC GAT AAA TTT GAA AAA TAC CTT AAT GAG CAT TCT TTT CCT GAA CCT 528
 Arg Asp Lys Phe Glu Lys Tyr Leu Asn Glu His Ser Phe Pro Glu Pro
 165 170 175
 TTT AGC GAT GGA AGT AGT GCT GAT AAA TTA GAT GAA GAT CTA AGC GAA 576
 Phe Ser Asp Gly Ser Ser Ala Asp Lys Leu Asp Glu Asp Leu Ser Glu
 180 185 190
 TCT GCA TAC ACA ACG AAC TCT GAT GCA TCA ATT GTT AAT GAC AGG GAC 624
 Ser Ala Tyr Thr Thr Asn Ser Asp Ala Ser Ile Val Asn Asp Arg Asp
 195 200 205
 TAC CAA GAA ACA GAT ATC GGC AAA CAT CCA AAG CTA CTG ATG TTT TTA 672
 Tyr Gln Glu Thr Asp Ile Gly Lys His Pro Lys Leu Leu Met Phe Leu
 210 215 220
 CCA ATT GAG CTT AAA TTT AGC CGC GGT TCC CTA CTG TTA GGA AAC AAA 720
 Pro Ile Glu Leu Lys Phe Ser Arg Gly Ser Leu Leu Leu Gly Asn Lys
 225 230 235 240
 TTC ACG CCA TCT GTT ATG ATT CTA AGT TAT GAA AGT GGA AAA GGC ATA 768
 Phe Thr Pro Ser Val Met Ile Leu Ser Tyr Glu Ser Gly Lys Gly Ile
 245 250 255
 ATA GAT GTT TTA CCT CCA AAA GAG CGA TTA GAT TTA TAC AGA AAT AAA 816
 Ile Asp Val Leu Pro Pro Lys Glu Arg Leu Asp Leu Tyr Arg Asn Lys
 260 265 270
 ACA CAG ATG GAA TTC AAA AAC TTC GAA ATT TCT ATC AAA CAA AAT ATT 864
 Thr Gln Met Glu Phe Lys Asn Phe Glu Ile Ser Ile Lys Gln Asn Ile
 275 280 285
 GGT TAC GAT GAT GCT ATT GGA TTG AAG TTT AAA ATA GAT AGA GGG AAA 912
 Gly Tyr Asp Asp Ala Ile Gly Leu Lys Phe Lys Ile Asp Arg Gly Lys

290	295	300	
GTG TCA AAG TTA TGG AAA ACG TTT GTA CGA GTC TTT CAG ATA GTA ACC			960
Val Ser Lys Leu Trp Lys Thr Phe Val Arg Val Phe Gln Ile Val Thr			
305	310	315	320
AAG CCT GTT GTA CCG AAA AAG ACT AAA AAA AGC GCA GGC ACA TCA GAT			1008
Lys Pro Val Val Pro Lys Lys Thr Lys Lys Ser Ala Gly Thr Ser Asp			
325	330	335	
GAC AAT TTC TAT CAT AAA TGG AAA GGT TTA TCT CTT TAT AAG GCT TCT			1056
Asp Asn Phe Tyr His Lys Trp Lys Gly Leu Ser Leu Tyr Lys Ala Ser			
340	345	350	
GCG GGC GAC GCT AAA GCA AGT GAT TTA GAT GAT GTT GAG TTC GAT TTG			1104
Ala Gly Asp Ala Lys Ala Ser Asp Leu Asp Asp Val Glu Phe Asp Leu			
355	360	365	
ACG AAC CAT GAA TAT GCT AAA TTT ACA TCA ATT TTA AAA TGC CCA AAG			1152
Thr Asn His Glu Tyr Ala Lys Phe Thr Ser Ile Leu Lys Cys Pro Lys			
370	375	380	
GTC ACA ATT GCA TAT GAC GTG GAT GTT CCG GGC GTT GTG CCA CAT GGT			1200
Val Thr Ile Ala Tyr Asp Val Asp Val Pro Gly Val Val Pro His Gly			
385	390	395	400
GCA CAT CCG ACA ATA CCT GAT ATT GAT GGA CCA GAT GTG GGC AAT AAC			1248
Ala His Pro Thr Ile Pro Asp Ile Asp Gly Pro Asp Val Gly Asn Asn			
405	410	415	
GGA GCA CCT CCA GAT TTT GCT TTA GAT GTT CAA ATT CAC GGA GGA TCC			1296
Gly Ala Pro Pro Asp Phe Ala Leu Asp Val Gln Ile His Gly Gly Ser			
420	425	430	
ATC TGT TAC GGA CCT TGG GCT CAA AGA CAA GTC AGT CAT CTA CAA AGA			1344
Ile Cys Tyr Gly Pro Trp Ala Gln Arg Gln Val Ser His Leu Gln Arg			
435	440	445	
GTT CTA TCA CCG GTA GTT TCA AGG ACA GCC AAA CCT ATA AAA AAA CTC			1392

Val Leu Ser Pro Val Val Ser Arg Thr Ala Lys Pro Ile Lys Lys Leu
 450 455 460
 CCG CCA GGT TCT AGA AGA ATA TAT ACA CTT TTC AGG ATG AAT ATA TCA 1440
 Pro Pro Gly Ser Arg Arg Ile Tyr Thr Leu Phe Arg Met Asn Ile Ser
 465 470 475 480
 ATA ATG GAA GAT ACT ACT TGG CGT ATA CCG ACG AGG GAA AGT AGC AAA 1488
 Ile Met Glu Asp Thr Thr Trp Arg Ile Pro Thr Arg Glu Ser Ser Lys
 485 490 495
 GAC CCC GAA TTT TTG AAA CAC TAC AAA GAA ACT AAT GAA GAA TAT AGG 1536
 Asp Pro Glu Phe Leu Lys His Tyr Lys Glu Thr Asn Glu Glu Tyr Arg
 500 505 510
 CCA TTT GGA TGG ATG GAT CTC CGA TTT TGT AAG GAC ACC TAT GCA AAT 1584
 Pro Phe Gly Trp Met Asp Leu Arg Phe Cys Lys Asp Thr Tyr Ala Asn
 515 520 525
 TTC AAT ATA AGT GTT TGT CCT ACA GTG CAA GGT TTT CAG AAT AAT TTC 1632
 Phe Asn Ile Ser Val Cys Pro Thr Val Gln Gly Phe Gln Asn Asn Phe
 530 535 540
 CAT GTT CAT TTC CTG GAA ACC GAA ATT AGG TCA AGT GTT AAT CAC GAT 1680
 His Val His Phe Leu Glu Thr Glu Ile Arg Ser Ser Val Asn His Asp
 545 550 555 560
 ATT TTG TTA AAA AGC AAG GTA TTC GAT ATT GAT GGG GAT ATT GGA TAT 1728
 Ile Leu Leu Lys Ser Lys Val Phe Asp Ile Asp Gly Asp Ile Gly Tyr
 565 570 575
 CCA TTG GGT TGG AAT AGC AAA GCT ATA TGG ATA ATT AAC ATG AAG TCA 1776
 Pro Leu Gly Trp Asn Ser Lys Ala Ile Trp Ile Ile Asn Met Lys Ser
 580 585 590
 GAA CAA TTA GAG GCG TTT CTG CTA CGT GAG CAT ATA ACT TTA GTT GCA 1824
 Glu Gln Leu Glu Ala Phe Leu Leu Arg Glu His Ile Thr Leu Val Ala
 595 600 605

GAT ACG CTT TCA GAC TTT TCC GCT GGT GAT CCT ACG CCT TAC GAA CTT 1872
 Asp Thr Leu Ser Asp Phe Ser Ala Gly Asp Pro Thr Pro Tyr Glu Leu
 610 615 620
 TTT AGA CCA TTC GTA TAC AAA GTC AAT TGG GAA ATG GAA GGA TAT TCC 1920
 Phe Arg Pro Phe Val Tyr Lys Val Asn Trp Glu Met Glu Gly Tyr Ser
 625 630 635 640
 ATT TAC TTA AAC GTC AAT GAT CAC AAT ATT GTT AAC AAT CCG TTA GAT 1968
 Ile Tyr Leu Asn Val Asn Asp His Asn Ile Val Asn Asn Pro Leu Asp
 645 650 655
 TTT AAC GAA AAC TGT TAT TTA TCC CTT CAT GGT GAT AAG CTT TCA ATT 2016
 Phe Asn Glu Asn Cys Tyr Leu Ser Leu His Gly Asp Lys Leu Ser Ile
 660 665 670
 GAT GTC ACG GTA CCC CGT GAG AGT ATT TTG GGG ACA TAC ACA GAT ATG 2064
 Asp Val Thr Val Pro Arg Glu Ser Ile Leu Gly Thr Tyr Thr Asp Met
 675 680 685
 TCC TAC GAG ATC TCA ACT CCA ATG TTC AGA ATG ATG TTA AAT ACC CCC 2112
 Ser Tyr Glu Ile Ser Thr Pro Met Phe Arg Met Met Leu Asn Thr Pro
 690 695 700
 CCT TGG AAT ACA TTG AAC GAA TTC ATG AAA CAT AAA GAA GTG GGG AGA 2160
 Pro Trp Asn Thr Leu Asn Glu Phe Met Lys His Lys Glu Val Gly Arg
 705 710 715 720
 GCA TAC GAC TTT ACA ATT AAA GGT TCT TAC CTT CTC TAT TCC GAG TTA 2208
 Ala Tyr Asp Phe Thr Ile Lys Gly Ser Tyr Leu Leu Tyr Ser Glu Leu
 725 730 735
 GAT ATT GAT AAT GTC GAT ACG CTA GTC ATA GAG TGT AAC AGC AAG AGT 2256
 Asp Ile Asp Asn Val Asp Thr Leu Val Ile Glu Cys Asn Ser Lys Ser
 740 745 750
 ACA GTA CTT CAC TGC TAT GGG TTT GTC ATG AGG TAT TTA ACA AAC GTA 2304
 Thr Val Leu His Cys Tyr Gly Phe Val Met Arg Tyr Leu Thr Asn Val

755	760	765	
AAG ATG AAT TAC TTC GGT GAA TTT TTT AAT TTT GTG ACG TCA GAA GAG	2352		
Lys Met Asn Tyr Phe Gly Glu Phe Phe Asn Phe Val Thr Ser Glu Glu			
770	775	780	
TAC ACA GGT GTC CTT GGC GCT AGG GAA GTC GGA GAT GTC ACT ACG AAA	2400		
Tyr Thr Gly Val Leu Gly Ala Arg Glu Val Gly Asp Val Thr Thr Lys			
785	790	795	800
AGC TCG GTG GCA GAT TTG GCA TCT ACT GTA GAT TCA GGG TAC CAA AAT	2448		
Ser Ser Val Ala Asp Leu Ala Ser Thr Val Asp Ser Gly Tyr Gln Asn			
805	810	815	
AGC AGT CTA AAG AAC GAA TCT GAG GAT AAA GGT CCT ATG AAA AGG TCA	2496		
Ser Ser Leu Lys Asn Glu Ser Glu Asp Lys Gly Pro Met Lys Arg Ser			
820	825	830	
GAT TTG AAA AGG ACT ACC AAC GAA ACT GAT ATT TGG TTC ACA TTT TCG	2544		
Asp Leu Lys Arg Thr Thr Asn Glu Thr Asp Ile Trp Phe Thr Phe Ser			
835	840	845	
GTT TGG GAT GGT GCT CTG ATA TTA CCA GAA ACG ATT TAC AGT TTT GAT	2592		
Val Trp Asp Gly Ala Leu Ile Leu Pro Glu Thr Ile Tyr Ser Phe Asp			
850	855	860	
CCA TGC ATT GCA CTA CAT TTT GCC GAA CTT GTA GTG GAT TTC AGA AGT	2640		
Pro Cys Ile Ala Leu His Phe Ala Glu Leu Val Val Asp Phe Arg Ser			
865	870	875	880
TGT AAT TAT TAT ATG GAC ATA ATG GCG GTT CTC AAC GGG ACT TCA ATA	2688		
Cys Asn Tyr Tyr Met Asp Ile Met Ala Val Leu Asn Gly Thr Ser Ile			
885	890	895	
AAG CGG CAC GTT TCA AAA CAA ATA AAT GAA GTA TTT GAT TTT ATA CGT	2736		
Lys Arg His Val Ser Lys Gln Ile Asn Glu Val Phe Asp Phe Ile Arg			
900	905	910	
CGT AAT AAC GGA GCT GAT GAG CAA GAG CAC GGA TTG CTT TCG GAC CTC	2784		

Arg Asn Asn Gly Ala Asp Glu Gln Glu His Gly Leu Leu Ser Asp Leu
 915 920 925
 ACC ATT CAT GGA CAT AGA ATG TAT GGA TTA CCA CCC ACA GAA CCT ACC 2832
 Thr Ile His Gly His Arg Met Tyr Gly Leu Pro Pro Thr Glu Pro Thr
 930 935 940
 TAC TTT TGT CAA TGG GAT ATC AAT CTC GGA GAT TTA TGC ATT GAT TCA 2880
 Tyr Phe Cys Gln Trp Asp Ile Asn Leu Gly Asp Leu Cys Ile Asp Ser
 945 950 955 960
 GAT ATT GAA TTT ATA AAG GGA TTC TTT AAT TCC TTT TAT AAG ATA GGT 2928
 Asp Ile Glu Phe Ile Lys Gly Phe Phe Asn Ser Phe Tyr Lys Ile Gly
 965 970 975
 TTT GGC TAC AAT GAC TTG GAA AAT ATA TTA TTA TAT GAC ACT GAG ACC 2976
 Phe Gly Tyr Asn Asp Leu Glu Asn Ile Leu Leu Tyr Asp Thr Glu Thr
 980 985 990
 ATT AAT GAT ATG ACC TCG CTA ACC GTG CAC GTT GAA AAA ATA AGA ATA 3024
 Ile Asn Asp Met Thr Ser Leu Thr Val His Val Glu Lys Ile Arg Ile
 995 1000 1005
 GGC CTT AAA GAT CCG GTG ATG AAA TCT CAA TCA GTT ATT AGT GCT GAA 3072
 Gly Leu Lys Asp Pro Val Met Lys Ser Gln Ser Val Ile Ser Ala Glu
 1010 1015 1020
 TCG ATA TTG TTT ACT TTG ATC GAC TTT GAA AAC GAA AAA TAT TCA CAA 3120
 Ser Ile Leu Phe Thr Leu Ile Asp Phe Glu Asn Glu Lys Tyr Ser Gln
 1025 1030 1035 1040
 AGA ATA GAC GTG AAA ATT CCA AAA TTG ACA ATT TCG TTA AAT TGC GTG 3168
 Arg Ile Asp Val Lys Ile Pro Lys Leu Thr Ile Ser Leu Asn Cys Val
 1045 1050 1055
 ATG GGC GAT GGC GTA GAC ACA TCA TTT CTC AAA TTC GAA ACA AAA TTA 3216
 Met Gly Asp Gly Val Asp Thr Ser Phe Leu Lys Phe Glu Thr Lys Leu
 1060 1065 1070

AGA TTT ACA AAC TTT GAG CAA TAC AAG GAT ATC GAT AAA AAA AGA TCA 3264
 Arg Phe Thr Asn Phe Glu Gln Tyr Lys Asp Ile Asp Lys Lys Arg Ser
 1075 1080 1085
 GAA CAA CGC AGA TAT ATA ACA ATA CAC GAT TCA CCC TAT CAT AGG TGT 3312
 Glu Gln Arg Arg Tyr Ile Thr Ile His Asp Ser Pro Tyr His Arg Cys
 1090 1095 1100
 CCT TTT CTT CTT CCG CTG TTC TAT CAG GAT TCG GAT ACA TAC CAA AAC 3360
 Pro Phe Leu Leu Pro Leu Phe Tyr Gln Asp Ser Asp Thr Tyr Gln Asn
 1105 1110 1115 1120
 CTG TAC GGG GCT ATA GCA CCA TCT TCG TCT ATC CCA ACT TTA CCT CTT 3408
 Leu Tyr Gly Ala Ile Ala Pro Ser Ser Ser Ile Pro Thr Leu Pro Leu
 1125 1130 1135
 CCC ACT TTG CCT GAT ACT ATA GAT TAT ATC ATT GAA GAT ATT GTG GGC 3456
 Pro Thr Leu Pro Asp Thr Ile Asp Tyr Ile Ile Glu Asp Ile Val Gly
 1140 1145 1150
 GAG TAT GCT ACC CTT CTG GAG ACC ACA AAT CCA TTC AAG AAC ATA TTC 3504
 Glu Tyr Ala Thr Leu Leu Glu Thr Thr Asn Pro Phe Lys Asn Ile Phe
 1155 1160 1165
 GCA GAA ACT CCA TCA ACT ATG GAG CCT TCA AGA GCC AGC TTC AGT GAA 3552
 Ala Glu Thr Pro Ser Thr Met Glu Pro Ser Arg Ala Ser Phe Ser Glu
 1170 1175 1180
 GAT GAT AAT GAC GAA GAA GCG GAC CCT TCA AGC TTC AAA CCT GTC GCT 3600
 Asp Asp Asn Asp Glu Glu Ala Asp Pro Ser Ser Phe Lys Pro Val Ala
 1185 1190 1195 1200
 TTT ACA GAA GAC AGA AAC CAC GAA AGG GAT AAC TAT GTT GTT GAT GTT 3648
 Phe Thr Glu Asp Arg Asn His Glu Arg Asp Asn Tyr Val Val Asp Val
 1205 1210 1215
 TCA TAT ATT CTG TTG GAT GTC GAC CCG TTG CTT TTT ATT TTC GCT AAG 3696
 Ser Tyr Ile Leu Leu Asp Val Asp Pro Leu Leu Phe Ile Phe Ala Lys

1220	1225	1230	
AGT TTA TTA GAA CAG CTT TAC TCT GAA AAC ATG GTA CAA GTC TTA GAC			3744
Ser Leu Leu Glu Gln Leu Tyr Ser Glu Asn Met Val Gln Val Leu Asp			
1235	1240	1245	
GAT ATT GAA ATT GGG ATT GTG AAA CGA TTA AGC AAC CTT CAA GAA GGG			3792
Asp Ile Glu Ile Gly Ile Val Lys Arg Leu Ser Asn Leu Gln Glu Gly			
1250	1255	1260	
ATC ACT TCT ATT TCA AAC ATT GAT ATC CAT ATT GCT TAT CTA AAT TTA			3840
Ile Thr Ser Ile Ser Asn Ile Asp Ile His Ile Ala Tyr Leu Asn Leu			
1265	1270	1275	1280
ATC TGG CAA GAG ACA GGT GAG GAA GGT TTT GAG CTC TAT TTA GAT CGT			3888
Ile Trp Gln Glu Thr Gly Glu Glu Gly Phe Glu Leu Tyr Leu Asp Arg			
1285	1290	1295	
ATT GAT TAT CAA ATG AGT GAA AAG TCT CTA GAG AAG AAC CGA ACA AAT			3936
Ile Asp Tyr Gln Met Ser Glu Lys Ser Leu Glu Lys Asn Arg Thr Asn			
1300	1305	1310	
AAA TTA TTA GAA GTA GCA GCT TTA GCA AAG GTA AAA ACT GTC AGA GTG			3984
Lys Leu Leu Glu Val Ala Ala Leu Ala Lys Val Lys Thr Val Arg Val			
1315	1320	1325	
ACT GTT AAC CAG AAG AAA AAT CCA GAC TTG TCT GAA GAT CGT CCC CCT			4032
Thr Val Asn Gln Lys Lys Asn Pro Asp Leu Ser Glu Asp Arg Pro Pro			
1330	1335	1340	
GCA CTG TCG CTA GGG ATT GAG GGT TTC GAA GTA TGG TCT TCT ACA GAA			4080
Ala Leu Ser Leu Gly Ile Glu Gly Phe Glu Val Trp Ser Ser Thr Glu			
1345	1350	1355	1360
GAT AGA CAA GTT AAC TCA TTA AAC TTA ACG TCA TCA GAT ATT ACC ATA			4128
Asp Arg Gln Val Asn Ser Leu Asn Leu Thr Ser Ser Asp Ile Thr Ile			
1365	1370	1375	
GAC GAA TCT CAA ATG GAA TGG CTG TTT GAG TAC TGT AGT GAC CAG GGA			4176

Asp Glu Ser Gln Met Glu Trp Leu Phe Glu Tyr Cys Ser Asp Gln Gly
 1380 1385 1390
 AAT CTT ATT CAA GAG GTT TGC ACT TCT TTT AAT TCT ATT CAG AAC ACC 4224
 Asn Leu Ile Gln Glu Val Cys Thr Ser Phe Asn Ser Ile Gln Asn Thr
 1395 1400 1405
 AGA AGT AAT TCA AAG ACA GAA CTC ATT TCA AAG CTC ACA GCC GCA AGC 4272
 Arg Ser Asn Ser Lys Thr Glu Leu Ile Ser Lys Leu Thr Ala Ala Ser
 1410 1415 1420
 GAA TAT TAT CAA ATT AGT CAT GAT CCT TAC GTC ATA ACA AAA CCT GCT 4320
 Glu Tyr Tyr Gln Ile Ser His Asp Pro Tyr Val Ile Thr Lys Pro Ala
 1425 1430 1435 1440
 TTT ATT ATG AGA CTT TCC AAA GGG CAT GTG CGT GAG AAT CGT AGT TGG 4368
 Phe Ile Met Arg Leu Ser Lys Gly His Val Arg Glu Asn Arg Ser Trp
 1445 1450 1455
 AAA ATT ATT ACG CGT CTG AGA CAC ATT TTA ACG TAC CTT CCT GAT GAT 4416
 Lys Ile Ile Thr Arg Leu Arg His Ile Leu Thr Tyr Leu Pro Asp Asp
 1460 1465 1470
 TGG CAA AGC AAC ATC GAC GAA GTG CTA AAA GAA AAG AAA TAT ACC TCT 4464
 Trp Gln Ser Asn Ile Asp Glu Val Leu Lys Glu Lys Lys Tyr Thr Ser
 1475 1480 1485
 GCT AAA GAT GCA AAA AAT ATC TTC ATG TCT GTG TTT TCG ACT TGG AGA 4512
 Ala Lys Asp Ala Lys Asn Ile Phe Met Ser Val Phe Ser Thr Trp Arg
 1490 1495 1500
 AAT TGG GAG TTC TCA GAT GTT GCA AGG TCG TAT ATA TAC GGC AAA TTA 4560
 Asn Trp Glu Phe Ser Asp Val Ala Arg Ser Tyr Ile Tyr Gly Lys Leu
 1505 1510 1515 1520
 TTC ACG GCA GAA AAT GAG AAA CAT AAA CAA AAT TTG ATT AAA AAA TTG 4608
 Phe Thr Ala Glu Asn Glu Lys His Lys Gln Asn Leu Ile Lys Lys Leu
 1525 1530 1535

TTG AAG TGT ACC ATG GGA TCA TTT TAC CTT ACT GTT TAT GGT GAG GGA 4656
 Leu Lys Cys Thr Met Gly Ser Phe Tyr Leu Thr Val Tyr Gly Glu Gly
 1540 1545 1550
 TAT GAG GTT GAG CAT AAT TTT GTT GTT GCG GAT GCC AAT CTG GTA GTG 4704
 Tyr Glu Val Glu His Asn Phe Val Val Ala Asp Ala Asn Leu Val Val
 1555 1560 1565
 GAT TTG ACG CCT CCG GTG ACA AGC TTA CCT TCA AAT CGA GAA GAA ACT 4752
 Asp Leu Thr Pro Pro Val Thr Ser Leu Pro Ser Asn Arg Glu Glu Thr
 1570 1575 1580
 ATT GAA ATT ACG GGA AGA GTA GGC TCA GTA AAA GGA AAA TTC AGT GAT 4800
 Ile Glu Ile Thr Gly Arg Val Gly Ser Val Lys Gly Lys Phe Ser Asp
 1585 1590 1595 1600
 AGG TTA CTT AAA TTG CAA GAT CTT ATT CCA CTC ATT GCA GCA GTG GGC 4848
 Arg Leu Leu Lys Leu Gln Asp Leu Ile Pro Leu Ile Ala Ala Val Gly
 1605 1610 1615
 GAA GAT GAC AAA AGT GAT CCA AAA AAG GAG TTA TCA AAG CAA TTC AAA 4896
 Glu Asp Asp Lys Ser Asp Pro Lys Lys Glu Leu Ser Lys Gln Phe Lys
 1620 1625 1630
 ATG AAC ACC GTT TTA TTA GTG GAT AAA AGT GAA CTG CAA CTG GTC ATG 4944
 Met Asn Thr Val Leu Leu Val Asp Lys Ser Glu Leu Gln Leu Val Met
 1635 1640 1645
 GAC CAA ACG AAG CTG ATG AGT AGA ACA GTT GGG GGT AGA GTT AGT TTA 4992
 Asp Gln Thr Lys Leu Met Ser Arg Thr Val Gly Gly Arg Val Ser Leu
 1650 1655 1660
 CTA TGG GAA AAT CTA AAA GAT TCA ACT AGT CAA GCG GGT TCA TTG GTT 5040
 Leu Trp Glu Asn Leu Lys Asp Ser Thr Ser Gln Ala Gly Ser Leu Val
 1665 1670 1675 1680
 ATA TTT TCC CAG AAA TCG GAA GTG TGG TTA AAA CAC ACA TCT GTC ATT 5088
 Ile Phe Ser Gln Lys Ser Glu Val Trp Leu Lys His Thr Ser Val Ile

1685	1690	1695	
TTG GGA GAA GCT CAA CTG CGC GAC TTT TCA GTT TTA GCG ACT ACT GAG	5136		
Leu Gly Glu Ala Gln Leu Arg Asp Phe Ser Val Leu Ala Thr Thr Glu			
1700	1705	1710	
GCA TGG TCA CAC AAG CCT ACG ATT CTG ATA AAC AAC CAG TGC GCA GAT	5184		
Ala Trp Ser His Lys Pro Thr Ile Leu Ile Asn Asn Gln Cys Ala Asp			
1715	1720	1725	
CTT CAT TTT AGA GCA ATG AGT TCA ACT GAG CAA TTA GTA ACC GCT ATT	5232		
Leu His Phe Arg Ala Met Ser Ser Thr Glu Gln Leu Val Thr Ala Ile			
1730	1735	1740	
ACT GAA ATT AGG GAA AGT CTG ATG ATG ATT AAA GAG CGC ATA AAG TTT	5280		
Thr Glu Ile Arg Glu Ser Leu Met Met Ile Lys Glu Arg Ile Lys Phe			
1745	1750	1755	1760
AAA CCT AAA TCA AAG AAA AAG TCC CAA TTT GTC GAC CAG AAA ATT AAT	5328		
Lys Pro Lys Ser Lys Lys Lys Ser Gln Phe Val Asp Gln Lys Ile Asn			
1765	1770	1775	
ACA GTC TTG TCA TGT TAT TTT TCA AAC GTT AGT TCT GAA GTT ATG CCG	5376		
Thr Val Leu Ser Cys Tyr Phe Ser Asn Val Ser Ser Glu Val Met Pro			
1780	1785	1790	
CTC TCG CCA TTT TAT ATT CGT CAC GAA GCC AAG CAG CTT GAT ATA TAT	5424		
Leu Ser Pro Phe Tyr Ile Arg His Glu Ala Lys Gln Leu Asp Ile Tyr			
1795	1800	1805	
TTT AAC AAA TTC GGT TCA AAT GAG ATT TTG TTA AGC ATA TGG GAT ACT	5472		
Phe Asn Lys Phe Gly Ser Asn Glu Ile Leu Leu Ser Ile Trp Asp Thr			
1810	1815	1820	
GAT TTT TTC ATG ACA TCG CAC CAG ACA AAG GAG CAA TAC CTA AGG TTT	5520		
Asp Phe Phe Met Thr Ser His Gln Thr Lys Glu Gln Tyr Leu Arg Phe			
1825	1830	1835	1840
TCA TTT GGC GAT ATT GAA ATT AAA GGA GGA ATT TCT AGA GAA GGC TAT	5568		

Ser Phe Gly Asp Ile Glu Ile Lys Gly Gly Ile Ser Arg Glu Gly Tyr
 1845 1850 1855
 TCG TTG ATA AAC GTT GAC ATC TCA ATA TCT ATG ATT AAG TTA ACC TTT 5616
 Ser Leu Ile Asn Val Asp Ile Ser Ile Ser Met Ile Lys Leu Thr Phe
 1860 1865 1870
 TCG GAG CCG CGC CGT ATT GTA AAC AGT TTT TTA CAA GAT GAA AAG CTT 5664
 Ser Glu Pro Arg Arg Ile Val Asn Ser Phe Leu Gln Asp Glu Lys Leu
 1875 1880 1885
 GCT TCT CAG GGT ATC AAT CTG TTA TAT TCC CTG AAG CCT TTA TTC TTT 5712
 Ala Ser Gln Gly Ile Asn Leu Leu Tyr Ser Leu Lys Pro Leu Phe Phe
 1890 1895 1900
 AGT TCA AAT CTA CCA AAA AAA GAG AAG CAG GCA CCC TCG ATA ATG ATA 5760
 Ser Ser Asn Leu Pro Lys Lys Glu Lys Gln Ala Pro Ser Ile Met Ile
 1905 1910 1915 1920
 AAT TGG ACA TTA GAT ACT AGC ATT ACT TAT TTT GGT GTT CTT GTG CCA 5808
 Asn Trp Thr Leu Asp Thr Ser Ile Thr Tyr Phe Gly Val Leu Val Pro
 1925 1930 1935
 GTG GCT TCC ACG TAT TTC GTG TTT GAA TTA CAT ATG CTG CTA CTT TCT 5856
 Val Ala Ser Thr Tyr Phe Val Phe Glu Leu His Met Leu Leu Leu Ser
 1940 1945 1950
 CTG ACC AAT ACG AAT AAC GGT ATG TTA CCA GAA GAA ACC AAG GTG ACG 5904
 Leu Thr Asn Thr Asn Asn Gly Met Leu Pro Glu Glu Thr Lys Val Thr
 1955 1960 1965
 GGA CAG TTT TCC ATC GAA AAC ATC CTA TTT CTA ATA AAG GAG CGG TCA 5952
 Gly Gln Phe Ser Ile Glu Asn Ile Leu Phe Leu Ile Lys Glu Arg Ser
 1970 1975 1980
 CTA CCC ATT GGT CTT TCC AAA TTA CTC GAC TTT TCC ATA AAA GTA TCA 6000
 Leu Pro Ile Gly Leu Ser Lys Leu Leu Asp Phe Ser Ile Lys Val Ser
 1985 1990 1995 2000

ACC CTA CAA AGA ACG GTT GAT ACG GAG CAG TCA TTC CAA GTG GAA AGT	6048
Thr Leu Gln Arg Thr Val Asp Thr Glu Gln Ser Phe Gln Val Glu Ser	
2005 2010 2015	
TCT CAT TTC AGG GTC TGC TTA TCT CCT GAT TCT CTA TTA AGA TTA ATG	6096
Ser His Phe Arg Val Cys Leu Ser Pro Asp Ser Leu Leu Arg Leu Met	
2020 2025 2030	
TGG GGC GCG CAT AAA TTG CTA GAC TTG AGC CAT TAC TAT TCA AGA CGC	6144
Trp Gly Ala His Lys Leu Leu Asp Leu Ser His Tyr Tyr Ser Arg Arg	
2035 2040 2045	
CAT GCC CCT AAT ATT TGG AAC ACT AAG ATG TTC ACC GGT AAA AGT GAT	6192
His Ala Pro Asn Ile Trp Asn Thr Lys Met Phe Thr Gly Lys Ser Asp	
2050 2055 2060	
AAG TCA AAA GAA ATG CCC ATA AAT TTC CGT TCA ATA CAC ATC CTG TCC	6240
Lys Ser Lys Glu Met Pro Ile Asn Phe Arg Ser Ile His Ile Leu Ser	
2065 2070 2075 2080	
TAT AAA TTT TGT ATT GGG TGG ATA TTC CAG TAT GGA GCA GGC TCC AAT	6288
Tyr Lys Phe Cys Ile Gly Trp Ile Phe Gln Tyr Gly Ala Gly Ser Asn	
2085 2090 2095	
CCT GGG TTA ATG TTA GGT TAT AAC AGA TTG TTT TCA GCA TAT GAA AAG	6336
Pro Gly Leu Met Leu Gly Tyr Asn Arg Leu Phe Ser Ala Tyr Glu Lys	
2100 2105 2110	
GAT TTT GGG AAA TTC ACA GTT GTG GAC GCT TTT TTC TCT GTT GCG AAT	6384
Asp Phe Gly Lys Phe Thr Val Val Asp Ala Phe Phe Ser Val Ala Asn	
2115 2120 2125	
GGT AAT ACC TCA AGC ACT TTT TTC TCT GAA GGA AAC GAG AAA GAC AAA	6432
Gly Asn Thr Ser Ser Thr Phe Phe Ser Glu Gly Asn Glu Lys Asp Lys	
2130 2135 2140	
TAT AAT AGA AGT TTC TTG CCA AAC ATG CAA ATA TCC TAC TGG TTC AAA	6480
Tyr Asn Arg Ser Phe Leu Pro Asn Met Gln Ile Ser Tyr Trp Phe Lys	

2145	2150	2155	2160	
AGA TGT GGT GAG TTG AAA GAT TGG TTT TTT AGA TTT CAT GGT GAA GCA	6528			
Arg Cys Gly Glu Leu Lys Asp Trp Phe Phe Arg Phe His Gly Glu Ala				
2165	2170	2175		
CTG GAT GTA AAC TTT GTC CCG TCA TTC ATG GAT GTC ATT GAG TCT ACT	6576			
Leu Asp Val Asn Phe Val Pro Ser Phe Met Asp Val Ile Glu Ser Thr				
2180	2185	2190		
TTA CAA TCC ATG CGA GCA TTT CAA GAG CTG AAA AAG AAC ATT CTG GAT	6624			
Leu Gln Ser Met Arg Ala Phe Gln Glu Leu Lys Lys Asn Ile Leu Asp				
2195	2200	2205		
GTG TCC GAG AGT TTG CGT GCG GAA AAT GAT AAT TCT TAT GCT AGT ACC	6672			
Val Ser Glu Ser Leu Arg Ala Glu Asn Asp Asn Ser Tyr Ala Ser Thr				
2210	2215	2220		
AGT GTC GAA AGT GCT TCG AGT AGT TTG GCT CCC TTT CTC GAT AAC ATT	6720			
Ser Val Glu Ser Ala Ser Ser Ser Leu Ala Pro Phe Leu Asp Asn Ile				
2225	2230	2235	2240	
AGA TCT GTT AAC TCA AAT TTC AAG TAT GAC GGT GGT GTA TTT AGG GTT	6768			
Arg Ser Val Asn Ser Asn Phe Lys Tyr Asp Gly Gly Val Phe Arg Val				
2245	2250	2255		
TAC ACG TAC GAA GAT ATT GAA ACC AAG AGT GAG CCA TCT TTT GAA ATA	6816			
Tyr Thr Tyr Glu Asp Ile Glu Thr Lys Ser Glu Pro Ser Phe Glu Ile				
2260	2265	2270		
AAA AGT CCA GTA GTC ACT ATA AAC TGT ACA TAT AAA CAT GAT GAA GAT	6864			
Lys Ser Pro Val Val Thr Ile Asn Cys Thr Tyr Lys His Asp Glu Asp				
2275	2280	2285		
AAA GTT AAG CCA CAT AAA TTC AGA ACA TTA ATC ACT GTC GAC CCA ACG	6912			
Lys Val Lys Pro His Lys Phe Arg Thr Leu Ile Thr Val Asp Pro Thr				
2290	2295	2300		
CAT AAT ACT TTG TAT GCG GGA TGT GCT CCT TTA TTA ATG GAA TTT TCT	6960			

His Asn Thr Leu Tyr Ala Gly Cys Ala Pro Leu Leu Met Glu Phe Ser
 2305 2310 2315 2320
 GAA AGT CTG CAA AAG ATG ATA AAG AAA CAT AGC ACC GAC GAA AAA CCA 7008
 Glu Ser Leu Gln Lys Met Ile Lys Lys His Ser Thr Asp Glu Lys Pro
 2325 2330 2335
 AAC TTT ACA AAA CCT TCT TCA CAG AAT GTT GAT TAT AAG CGA CTT TTG 7056
 Asn Phe Thr Lys Pro Ser Ser Gln Asn Val Asp Tyr Lys Arg Leu Leu
 2340 2345 2350
 GAT CAA TTT GAT GTG GCT GTA AAA CTA ACA TCA GCC AAG CAA CAG CTA 7104
 Asp Gln Phe Asp Val Ala Val Lys Leu Thr Ser Ala Lys Gln Gln Leu
 2355 2360 2365
 AGT TTG AGC TGT GAA CCA AAA GCT AAG GTT CAG GCA GAT GTT GGA TTT 7152
 Ser Leu Ser Cys Glu Pro Lys Ala Lys Val Gln Ala Asp Val Gly Phe
 2370 2375 2380
 GAA TCG TTT TTG TTC AGT ATG GCT ACC AAT GAG TTC GAC TCT GAA CAG 7200
 Glu Ser Phe Leu Phe Ser Met Ala Thr Asn Glu Phe Asp Ser Glu Gln
 2385 2390 2395 2400
 CCT TTG GAG TTT TCT TTA ACT CTA GAA CAC ACA AAA GCG TCC ATT AAG 7248
 Pro Leu Glu Phe Ser Leu Thr Leu Glu His Thr Lys Ala Ser Ile Lys
 2405 2410 2415
 CAC ATA TTT TCA AGA GAA GTA AGT ACG TCC TTT GAA GTT GGT TTC ATG 7296
 His Ile Phe Ser Arg Glu Val Ser Thr Ser Phe Glu Val Gly Phe Met
 2420 2425 2430
 GAC TTG ACG CTT TTA TTT ACA CAT CCT GAT GTA ATC AGT ATG TAT GGA 7344
 Asp Leu Thr Leu Leu Phe Thr His Pro Asp Val Ile Ser Met Tyr Gly
 2435 2440 2445
 ACG GGG TTG GTT TCT GAT CTA AGC GTC TTC TTC AAT GTA AAG CAG CTC 7392
 Thr Gly Leu Val Ser Asp Leu Ser Val Phe Phe Asn Val Lys Gln Leu
 2450 2455 2460

CAG AAC CTG TAT TTA TTC TTG GAC ATA TGG AGG TTC AGT AGC ATT TTA 7440
 Gln Asn Leu Tyr Leu Phe Leu Asp Ile Trp Arg Phe Ser Ser Ile Leu
 2465 2470 2475 2480
 CAC ACA CGG CCA GTG CAA AGA ACT GTT AAT AAG GAA ATT GAA ATG AGT 7488
 His Thr Arg Pro Val Gln Arg Thr Val Asn Lys Glu Ile Glu Met Ser
 2485 2490 2495
 TCA TTA ACA TCA ACC AAC TAT GCC GAT GCA GGT ACG GAA ATA CCC TGG 7536
 Ser Leu Thr Ser Thr Asn Tyr Ala Asp Ala Gly Thr Glu Ile Pro Trp
 2500 2505 2510
 TGC TTT ACA TTA ATT TTT ACA AAT GTT AGC GGA GAC GTT GAT TTG GGT 7584
 Cys Phe Thr Leu Ile Phe Thr Asn Val Ser Gly Asp Val Asp Leu Gly
 2515 2520 2525
 CCT TCT CTC GGT ATG ATT TCA TTA AGG ACA CAA AGA ACA TGG CTG GCC 7632
 Pro Ser Leu Gly Met Ile Ser Leu Arg Thr Gln Arg Thr Trp Leu Ala
 2530 2535 2540
 ACA GAT CAT TAT AAC GAG AAG CGG CAG TTA CTG CAT GCT TTC ACT GAC 7680
 Thr Asp His Tyr Asn Glu Lys Arg Gln Leu Leu His Ala Phe Thr Asp
 2545 2550 2555 2560
 GGT ATT AGC TTG ACA TCA GAA GGT AGA CTG AGT GGT TTA TTT GAA GTT 7728
 Gly Ile Ser Leu Thr Ser Glu Gly Arg Leu Ser Gly Leu Phe Glu Val
 2565 2570 2575
 GCG AAT GCA AGT TGG TTA TCA GAA GTA AAA TGG CCA CCT GAA AAA AGC 7776
 Ala Asn Ala Ser Trp Leu Ser Glu Val Lys Trp Pro Pro Glu Lys Ser
 2580 2585 2590
 AAA AAT ACT CAT CCA TTA GTT TCC ACC TCC CTG AAT ATT GAT GAT ATA 7824
 Lys Asn Thr His Pro Leu Val Ser Thr Ser Leu Asn Ile Asp Asp Ile
 2595 2600 2605
 GCG GTA AAG GCT GCT TTT GAT TAT CAT ATG TTC TTA ATC GGC ACT ATA 7872
 Ala Val Lys Ala Ala Phe Asp Tyr His Met Phe Leu Ile Gly Thr Ile

2610	2615	2620	
AGT AAC ATA CAC TTC CAT CTT CAT AAT GAA AAG GAT GCC AAG GGG GTT			7920
Ser Asn Ile His Phe His Leu His Asn Glu Lys Asp Ala Lys Gly Val			
2625	2630	2635	2640
CTA CCT GAT TTG CTG CAG GTC TCT TTT TCA TCA GAT GAA ATT ATC CTC			7968
Leu Pro Asp Leu Leu Gln Val Ser Phe Ser Ser Asp Glu Ile Ile Leu			
2645	2650	2655	
AGC TCT ACT GCA TTA GTT GTA GCA AAT ATA CTG GAT ATC TAC AAC ACC			8016
Ser Ser Thr Ala Leu Val Val Ala Asn Ile Leu Asp Ile Tyr Asn Thr			
2660	2665	2670	
ATT GTA CGT ATG AGG CAG GAT AAT AAA ATA TCG TAT ATG GAG ACG TTG			8064
Ile Val Arg Met Arg Gln Asp Asn Lys Ile Ser Tyr Met Glu Thr Leu			
2675	2680	2685	
AGA GAT TCC AAT CCT GGT GAA TCT AGG CAA CCA ATA TTA TAC AAA GAC			8112
Arg Asp Ser Asn Pro Gly Glu Ser Arg Gln Pro Ile Leu Tyr Lys Asp			
2690	2695	2700	
ATT TTA AGA TCG CTG AAA TTA CTC AGA ACT GAT CTC TCG GTG AAT ATC			8160
Ile Leu Arg Ser Leu Lys Leu Leu Arg Thr Asp Leu Ser Val Asn Ile			
2705	2710	2715	2720
TCC TCT TCA AAG GTC CAG ATT TCG CCA ATA TCT TTA TTC GAT GTG GAA			8208
Ser Ser Ser Lys Val Gln Ile Ser Pro Ile Ser Leu Phe Asp Val Glu			
2725	2730	2735	
GTG TTA GTA ATA AGA ATT GAC AAA GTC TCT ATA CGT TCC GAA ACA CAT			8256
Val Leu Val Ile Arg Ile Asp Lys Val Ser Ile Arg Ser Glu Thr His			
2740	2745	2750	
TCG GGG AAA AAA TTA AAG ACA GAT TTG CAA CTA CAA GTT TTA GAT GTT			8304
Ser Gly Lys Lys Leu Lys Thr Asp Leu Gln Leu Gln Val Leu Asp Val			
2755	2760	2765	
TCT GCA GCG CTT TCT ACT TCC AAA GAA GAA TTA GAT GAG GAA GTT GGA			8352

Ser Ala Ala Leu Ser Thr Ser Lys Glu Glu Leu Asp Glu Glu Val Gly
 2770 2775 2780
 GCT TCC ATT GCT ATT GAT GAT TAC ATG CAT TAT GCT TCC AAG ATT GTC 8400
 Ala Ser Ile Ala Ile Asp Asp Tyr Met His Tyr Ala Ser Lys Ile Val
 2785 2790 2795 2800
 GGT GGT ACT ATC ATT GAT ATT CCA AAA CTT GCT GTT CAT ATG ACA ACT 8448
 Gly Gly Thr Ile Ile Asp Ile Pro Lys Leu Ala Val His Met Thr Thr
 2805 2810 2815
 TTA CAA GAA GAA AAG ACA AAT AAT TTA GAA TAT CTA TTT GCT TGC TCT 8496
 Leu Gln Glu Glu Lys Thr Asn Asn Leu Glu Tyr Leu Phe Ala Cys Ser
 2820 2825 2830
 TTT TCA GAC AAA ATA TCT GTA AGG TGG AAT CTA GGG CCT GTA GAC TTC 8544
 Phe Ser Asp Lys Ile Ser Val Arg Trp Asn Leu Gly Pro Val Asp Phe
 2835 2840 2845
 ATA AAG GAA ATG TGG ACT ACA CAT GTC AAA GCA CTG GCA GTT CGT CGA 8592
 Ile Lys Glu Met Trp Thr Thr His Val Lys Ala Leu Ala Val Arg Arg
 2850 2855 2860
 TCC CAG GTA GCA AAT ATT TCC TTT GGA CAA ACT GAG GAA GAA CTT GAA 8640
 Ser Gln Val Ala Asn Ile Ser Phe Gly Gln Thr Glu Glu Glu Leu Glu
 2865 2870 2875 2880
 GAA TCA ATT AAA AAG GAA GAA GCC GCT TCA AAG TTT AAT TAT ATT GCA 8688
 Glu Ser Ile Lys Lys Glu Glu Ala Ala Ser Lys Phe Asn Tyr Ile Ala
 2885 2890 2895
 CTA GAA GAA CCG CAG ATC GAA GTG CCT CAG ATA AGA GAT CTG GGA GAC 8736
 Leu Glu Glu Pro Gln Ile Glu Val Pro Gln Ile Arg Asp Leu Gly Asp
 2900 2905 2910
 GCC ACT CCA CCT ATG GAA TGG TTT GGT GTC AAT AGA AAA AAA TTT CCG 8784
 Ala Thr Pro Pro Met Glu Trp Phe Gly Val Asn Arg Lys Lys Phe Pro
 2915 2920 2925

AAA TTC ACT CAC CAA ACC GCA GTT ATC CCC GTC CAA AAG CTT GTT TAT 8832

Lys Phe Thr His Gln Thr Ala Val Ile Pro Val Gln Lys Leu Val Tyr

2930

2935

2940

CTT GCA GAA AAG CAG TAT GTC AAG ATA CTA GAT GAT ACG CAT 8874

Leu Ala Glu Lys Gln Tyr Val Lys Ile Leu Asp Asp Thr His

2945

2950

2955